

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) A system for determining a location of a target sequence in a genome sequence, comprising:
 - a storage unit storing a crosslink map, wherein the crosslink map comprises a-records for a sequence information for eachplurality of versions of a genome sequence comprising the sequence information;
 - an information search unit, for searching for identifier information and sequence information corresponding to a target sequence among the records in the crosslink map; and
 - a location estimation unit, for determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records,; calculating a difference value of a start position and an end position of athe reference sequence information obtained from the crosslink map,; and determining a location of the target sequence in athe genome sequence by a location shift corresponding to the difference value.
2. (Previously presented) The system of claim 1, further comprising an information integration unit, for receiving genome sequence data from various sources and transforming the received data into data formats recognized by the crosslink map.
3. (Previously presented) The system of claim 1, wherein a record for a sequence information in the crosslink map comprises
 - a name of a genome sequence,
 - a version of the genome sequence,
 - an identifier of a sequence information in the genome sequence,
 - a start position and an end position of the sequence information in the genome sequence, and

a length of the sequence information in the genome sequence.

4. (Currently amended) The system of claim 1, wherein the location estimation unit ~~determines the location of the target sequence by~~ is also for assigning a higher priority order to the calculated difference value for a ~~the~~ reference sequence information based on number of records for the reference sequence information ~~represented in the crosslink map by a larger number of records.~~

5. (Currently amended) The system of claim 1, wherein the location estimation unit comprises:

an estimation region setting portion for calculating a difference value of a start position and an end position of sequence information in the crosslink map excluded from the reference group and setting an estimation region for the location of the target sequence in the genome sequence based on the calculated difference value for sequence information; and

a location determining portion for determining the location of the target sequence in the estimation region of the genome sequence by a location shift corresponding to the calculated difference value for the reference sequence information.

6. (Previously presented) The system of claim 1, wherein the location estimation unit further comprises

an updating portion for updating the reference group, calculating a difference value of a start position and an end position for each sequence information in the updated reference group, and selecting sequence information in which the calculated difference value is within a predetermined range.

7. (Currently amended) A method of determining a location of a target sequence in a genome sequence, the method comprising:

inputting a target sequence;

searching for identifier information and sequence information corresponding to the target sequence in a crosslink map,

wherein the crosslink map comprises a-records for a sequence information for each plurality of versions of a genome sequence comprising the sequence information;

determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information ~~for an organism~~ is represented in the crosslink map by more than a predetermined number of records;

calculating a difference value of a start position and an end position of a-the reference sequence information obtained from the crosslink map; and

determining a location of the target sequence in a-the genome sequence by a location shift corresponding to the difference value; and

outputting the location of the target sequence in the genome sequence to a user.

8. (Previously presented) The method of claim 7, wherein a record for a sequence information recorded in the crosslink map comprises

a name of a genome sequence,

a version of the genome sequence,

an identifier for a sequence information in the genome sequence,

a start position and an end position of the sequence information in the genome sequence, and

a length of the sequence information in the genome sequence.

9. (Currently amended) The method of claim 7, wherein determining the location of the target sequence is carried out by

assigning a higher priority order to the difference value calculated for a-the reference sequence information represented based on number of records for the reference sequence information in the crosslink map by a larger number of records.

10. (Previously presented) The method of claim 7, further comprising
updating the reference group;
calculating a difference value of a start position and an end position for each sequence
information in the updated reference group; and
selecting sequence information in which the calculated difference value is within a
predetermined range.

11. (Currently amended) The method of claim 7, wherein determining the
location of the target genetic information comprises:
calculating a difference value of a start position and an end position of a sequence
information obtained from the crosslink map, wherein the sequence information was excluded
from the reference group;
setting an estimation region for the location of the target sequence on the genome
sequence based on the calculated difference value for the sequence information; and
determining the location of the target sequence in the estimation region of the genome
sequence by a location shift corresponding to the ~~calculated~~ difference value for the reference
sequence information.

12. (Currently amended) A computer readable medium having embodied thereon a computer program comprising computer readable code for executing the a method of determining a location of a target sequence in a genome sequence of claim 7, the method comprising

inputting a target sequence;

searching for identifier information and sequence information corresponding to the target sequence in a crosslink map,

wherein the crosslink map comprises records for a plurality of versions of a genome sequence;

determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records;

calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map;

determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value; and

outputting the location of the target sequence in the genome sequence to a user; and

wherein the computer readable medium is not a carrier wave.

13. – 14. (Cancelled)

15. (New) The system of claim 1, further comprising an output unit, for outputting the location of the target sequence in the genome sequence to a user.